



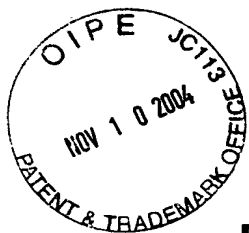
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## Fig.4 A

### Amino acid sequence of human gp130-Fc-His6

Sequence Range: 1 to 861

10	20	30	40	50	60
*	*	*	*	*	*
MVTLQTWVVQALFIFLT	TES	TGELLDPCGYISPESPVVQL	HSNFTAVCVLKEKCMDYFHV		
70	80	90	100	110	120
*	*	*	*	*	*
NANYIVWKTNHTIPKEQYT	IINRTASSVTFTDIASLNIQ	LTCNILTFGQLEQNVYGITI			
130	140	150	160	170	180
*	*	*	*	*	*
ISGLPPEKPKNLSCIVNEGK	KMRCEWDGGRETHLETNFTL	KSEWATHKFADCKAKRDTPT			
190	200	210	220	230	240
*	*	*	*	*	*
SCTVDYSTVYFVNIEVWVEA	ENALGKVTSDHINFDPVYKV	KPNPPHNLSVINSEELSSIL			
250	260	270	280	290	300
*	*	*	*	*	*
KLTWTNPSIKSVIILKYNIQ	YRTKDASTWSQIPPEDTAST	RSSFTVQDLKPFTEYVFRIR			
310	320	330	340	350	360
*	*	*	*	*	*
CMKEDGKGYWSDWSEEASGI	TYEDRPSKAPSFYKIDPSH	TQGYRTVQLVWKTLPPEAN			
370	380	390	400	410	420
*	*	*	*	*	*
GKILDYEVTLTRWKSHLQNY	TVNATKLTVNLTNDRYLATL	TVRNLVGKSDDAAVLTIPACD			
430	440	450	460	470	480
*	*	*	*	*	*
FQATHPVMDLKAFFKDNMLW	VEWTTTPRESVKKYILEWCVL	SDKAPCITDWQQEDGTVHRT			
490	500	510	520	530	540
*	*	*	*	*	*
YLRGNLAESKCYLITVTPVY	ADGPGSPESIKAYLKQAPPS	KGPTVTRTKKVGKNEAVLEWD			
550	560	570	580	590	600
*	*	*	*	*	*
QLPVDVQNGFIRNYTIFYRT	IIGNETAVNVDSSTHEYTLS	SLTSDTLYMVRMAAYTDEGG			
610	620	630	640	650	660
*	*	* ↑ ↑	*	*	*
KDGPEFTFTTPKFAQGEIES	<u>GEPKSCDKTHTCPPCPAPEL</u>	<u>LGGPSVLEFPPKPKDTLMIS</u>			
670	680	690	700	710	720
*	*	*	*	*	*
RTPEVTCVVVDVSHEDPEVK	<u>FNWYVDGVEVHNAKTKPREE</u>	<u>OYNSTYRVVSVLTVLHODWL</u>			
730	740	750	760	770	780
*	*	*	*	*	*



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Fig.4B

NGKEYKCKVSNKALPAPIEK TISKAKGOPREPOVYTLPPS RDELTKNOVSLTCLVKGFYP

790                      800                      810                      820                      830                      840  
\*                      \*                      \*                      \*                      \*                      \*

SDIAVEWESNGOPENNYKTT PPVLDSGSEFFLYSKLTVDK SRWOOGNVFSCSVMHEALHN

850                      860  
\*                      \*

HYTOKSLSLSPGKHHHHHH•

Fig.5.

The amino acid sequence of human IL-6R $\alpha$ -Fc

Sequence Range: 1 to 594

10                      20                      30                      40                      50                      60  
\*                      \*                      \*                      \*                      \*                      \*

MVAVGCALLAALLAAPGAAL APRRCPAQEVARGVLTSLPG DSVTLTCPGVEPEDNATVHW

70                      80                      90                      100                      110                      120  
\*                      \*                      \*                      \*                      \*                      \*

VLRKPAAGSHPSRWAGMGRR LLLRSVQLHDSGNYSYRAG RPAGTVHLLVDVPPEEPQLS

130                      140                      150                      160                      170                      180  
\*                      \*                      \*                      \*                      \*                      \*

CFRKSPLSNVVCEWGPRSTP SLTTKAVLLVRKFQNSPAED FQEPQCQYSQESQKFSCQLAV

190                      200                      210                      220                      230                      240  
\*                      \*                      \*                      \*                      \*                      \*

PEGDSSFYIVSMCVASSVGS KFSKTQTFQCGILQPDPPA NITVTAVARNPRWLSVTWQD

250                      260                      270                      280                      290                      300  
\*                      \*                      \*                      \*                      \*                      \*

PHSWNSSFYRLRFELRYRAE RSKTFTTWMVKDLQHHCVIH DAWSGLRHVQVQLRAQEEFGQ

310                      320                      330                      340                      350                      360  
\*                      \*                      \*                      \*                      \*                      \*

GEWSEWSPEAMGTPWTESRS PPAENEVSTPMQALTTNKDD DNILFRDSANATSLPVQDAG

370                      380                      390                      400                      410                      420  
\*†                      \*                      \*                      \*                      \*                      \*

EPKSCDKTHTCPPCPAPELL GGPSVLEFPKPKDTLMISR TPEVTCVVVDVSHEDPEVKF

430                      440                      450                      460                      470                      480  
\*                      \*                      \*                      \*                      \*                      \*

NWYVDGVEVHNAKTKPREEO YNSTYRVVSVLTVLHODWLN GKEYKCKVSNKALPAPIEKT

490                      500                      510                      520                      530                      540  
\*                      \*                      \*                      \*                      \*                      \*

ISKAKGOPREPOVYTLPPSR DELTKNOVSLTCLVKGFYPS DIAVEWESNGOPENNYKTT

550                      560                      570                      580                      590  
\*                      \*                      \*                      \*                      \*

PVLDSGSEFFLYSKLTVDKS RWOOGNVFSCSVMHEALHNH YTOKSLSLSPGK•

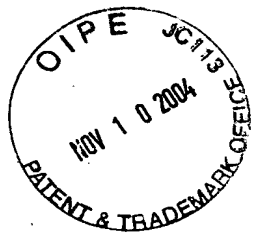
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# Fig.9A

## Amino acid sequence of gp130-Cy1

Sequence Range: 1 to 952

10	20	30	40	50	60
*	*	*	*	*	*
MVTLQTWVVQALFIFLTES	TGELLDP CGYISPESPVVQL	HSNFTA	VCVLKEK	CMDY	FHV
70	80	90	100	110	120
*	*	*	*	*	*
NANYIVWKTNHFTIPKEQYT	IINRTASSVTFTDIASLNIQ	LTCN	ILTFGQ	LEQN	VYGITI
130	140	150	160	170	180
*	*	*	*	*	*
ISGLPPEKPKNLSCIVNEGK	KMRCEWDG GRETHLETNFTL	KSEW	ATHKFAD	CKAKR	DTPT
190	200	210	220	230	240
*	*	*	*	*	*
SCTVDYSTVYFVNIEVWVEA	ENALGKVTS DHINFDPVYKV	KPNPP	HNLSVIN	SEEL	SSIL
250	260	270	280	290	300
*	*	*	*	*	*
KLTWINPSIKSVIILKYNIQ	YRTKDASTWSQIPPEDTAST	RSSFT	VQDLKP	FTEY	VFRIR
310	320	330	340	350	360
*	*	*	*	*	*
CMKEDGKGYWSDWSEEASGI	TYEDRPSKAPSFWKIDPSH	TQGY	RTVQLV	WKTL	PPFEAN
370	380	390	400	410	420
*	*	*	*	*	*
GKILDYEVTLTRWKSHLQNY	TVNATKLTVNLTNDRYLATL	TVRN	LVGKSD	AAVL	TIPACD
430	440	450	460	470	480
*	*	*	*	*	*
FQATHPVMDLKAFPKDNMLW	VEWTTPRESVKKYILEWCVL	SDKAP	CITDWQ	QEDGT	VHRT
490	500	510	520	530	540
*	*	*	*	*	*
YLRGNLAESKCYLITVTPVY	ADGPGSPESIKAYLKQAPPS	KGPT	VRTKKV	GKNEA	VLEWD
550	560	570	580	590	600
*	*	*	*	*	*
QLPVDVQNGFIRNYTIFYRT	IIGNETAVNVDSSHTEYTLS	SLTSD	TLYMVR	MAAYT	DEGG
610	620	630	640	650	660
*	*	*	*	*	*
KDGPEFTFTTPKFAQGEIES	<u>GASTKGPSVEPLAPSSKSTS</u>	<u>GGTAALGCLVKDYFPEP</u>	<u>VTV</u>		
670	680	690	700	710	720
*	*	*	*	*	*
<u>SWNSGALTSGVHTEPAVLOS</u>	<u>SGLYSLSSVVTVPSSSLGTO</u>	<u>TYICNVNHKPSNTKVDK</u>	<u>KVE</u>		
730	740	750	760	770	780
*	*	*	*	*	*
<u>PKSCDKTHTCPPCPAPELLG</u>	<u>GPSVFLEFPPKPKDTLMISRT</u>	<u>PEVTCVVVDVSHEDPEV</u>	<u>KFN</u>		



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Fig.9B

790	800	810	820	830	840
*	*	*	*	*	*
<u>WYVDGVEVHNAKTKPREEOY NSTYRVVSVLTVLHODWLNG KEYKCKVSNKALPAPLEKTI</u>					
850	860	870	880	890	900
*	*	*	*	*	*
<u>SKAKGOPREPOVYTLPPSRD ELTKNOVSLTCLVKGFYPSD IAVEWESNGOPENNYKTTTP</u>					
910	920	930	940	950	
*	*	*	*	*	
<u>VLDSGDSFFLYSKLTVDKSR WOOGNVFSCSVMHEALHNNHY TOKSLSLSPGK*</u>					

Fig.10.

Amino acid sequence of gp130Δ3fibro

Sequence Range: 1 to 332

10	20	30	40	50	60
*	*	*	*	*	*
MVTLQTWVVQALFIFLTES TGELLDPCGYISPESPVVQL HSNFTAVCVLKEKCMDYFHV					
70	80	90	100	110	120
*	*	*	*	*	*
NANYIVWKTNHFTIPKEQYT IINRTASSVTFTDIASLNIQ LTCNILTFGQLEQNVYGITI					
130	140	150	160	170	180
*	*	*	*	*	*
ISGLPPEKPKNLSCIVNEGK KMRCEWDGGRETHLETNFTL KSEWATHKFADCKAKRDTPT					
190	200	210	220	230	240
*	*	*	*	*	*
SCTVDYSTVYFVNIEVWVEA ENALGKVTSDHINFDPVYKV KPNPPHNLSVINSEELSSIL					
250	260	270	280	290	300
*	*	*	*	*	*
KLTWTNPSIKSVIILKYNIQ YRTKDASTWSQIPPEDTAST RSSFTVQDLKPFTEYVERIR					
310	320	330			
*	*	*			
CMKEDGKGYWSDWSEEASGI TYEDRPSKAPSG					